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CLMPTO

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1) A gamma subunit of a vertebrate AMP-activated kinase (AMPK), wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 70% identity with the polypeptide SEQ ID NO: 2.

2) A polypeptide of claim 1, wherein said polypeptide comprises a sequence having at least 95% identity with the polypeptide SEQ ID NO:2.

3) A polypeptide of claim 1, wherein said polypeptide comprises a sequence having at least 75% identity with the polypeptide SEQ ID NO: 28.

Claims 4 – 5 have been amended

-- 4) (Amended) A polypeptide of claim 1, wherein said polypeptide comprises the sequence of SEQ ID NO: 2 or SEQ ID NO:4.

5) (Amended) A polypeptide of claim 1, wherein said polypeptide comprises the sequence of SEQ ID NO: 28, SEQ ID NO: 30 or SEQ ID NO: 32.

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6) A polypeptide which is a functionally altered mutant of a gamma subunit of a vertebrate AMP-activated kinase, wherein said polypeptide has at least a mutation located within the first CBS domain of said gamma subunit.

7) A polypeptide of claim 6, wherein the mutation is located within the region of the first CBS domain aligned with the region of a polypeptide of SEQ ID NO: 2 spanning from residue 30 to residue 50.

8) A polypeptide of claim 7, wherein the mutation is a R→Q substitution or a V→I substitution.

Claims 9 – 11 have been amended

9) (Amended) A polypeptide of claim 8 selected from the group consisting of a polypeptide having a sequence resulting from a R→Q substitution at a position corresponding to position 41 of SEQ ID NO: 2;

and a polypeptide having a sequence resulting from a V→I substitution at the position corresponding to position 40 of SEQ ID NO: 2.

10) (Amended) A polypeptide which is a mutant of a gamma subunit of a vertebrate AMP-activated kinase, wherein said polypeptide results from a deletion of a part of a polypeptide of claim 1.

11) (Amended) A nucleic acid sequence encoding a polypeptide of claim 1, or the complement thereof, provided that said nucleic acid sequence does not consist of the EST GENBANK AA178898, or of the EST W94830.

12) A nucleic acid sequence of claim 11, having the sequence SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 27, SEQ ID NO: 29, SEQ ID NO: 31, or the complement thereof.

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Claims 13 – 26 have been amended

13) (Amended) A nucleic acid sequence comprising at least a portion of a nucleic acid sequence encoding a polypeptide of claim 1, and up to 500 kb of a 3' and/or of a 5' adjacent genomic DNA sequence, or the complement thereof.

14) (Amended) A nucleic acid fragment selected from the group consisting of:

a) a specific fragment of a nucleic acid sequence encoding a gamma subunit of a vertebrate AMPK, wherein said gamma subunit is a polypeptide comprising at least a sequence having at least 70% identity with the polypeptide SEQ ID NO: 2,

b) a specific fragment of a nucleic acid sequence encoding a polypeptide which is a functionally altered mutant of a gamma subunit of a vertebrate AMPK, wherein said polypeptide has at least a mutation located within the first CBS domain of said gamma subunit;

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c) a specific fragment of a nucleic acid sequence encoding a polypeptide which is a mutant of a gamma subunit of a vertebrate AMPK, wherein said polypeptide results from a deletion of a part of a polypeptide of a) or b);

d) a nucleic acid sequence comprising at least a portion of a nucleic acid sequence encoding a polypeptide of a), b), or c), and up to 500 kb of a 3' and/or of a 5' adjacent genomic DNA sequence, or the complement thereof; and

e) a nucleic acid fragment which specifically hybridizes under stringent conditions with a nucleic acid sequence of a), b), c), or d);

provided that said nucleic acid fragment does not consist of the EST GENBANK AA178898 or of the EST GENBANK W94830.

15) (Amended) A set of primers for amplifying a nucleic acid sequence, comprising a primer consisting of a nucleic acid fragment of claim 14.

16) (Amended) A recombinant vector comprising a nucleic acid sequence encoding a polypeptide of claim 1.

17) (Amended) A host cell transformed by a nucleic acid sequence encoding a polypeptide of claim 1.

18) (Amended) A transgenic animal transformed by a nucleic acid sequence encoding a polypeptide of claim 1.

19) (Amended) A knockout animal, wherein the gene encoding a polypeptide of claim 1 is inactive.

20) (Amended) A heterotrimeric AMPK wherein the  $\gamma$  subunit consists of a polypeptide of claim 1.

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21) (Amended) A method of detecting a metabolic disorder resulting from a mutation in a gene encoding a  $\gamma$  subunit of AMPK, wherein said process comprises:

- a) obtaining a nucleic acid sample from a vertebrate; and
- b) checking the presence in said nucleic acid of a nucleic acid sequence encoding a polypeptide of claim 1, wherein said polypeptide is functionally altered.

22) (Amended) A method of claim 21 wherein the disorder is correlated with an altered glycogen accumulation in the muscular cells and results from the expression of a functionally altered allele of a polypeptide, wherein said polypeptide comprises a sequence of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:28, SEQ ID NO:30, or SEQ ID NO:32.

23) (Amended) A method of claim 22 wherein the presence of the nucleic acid sequence encoding said mutant polypeptide is checked by contacting said nucleic acid sample with a nucleic acid probe spanning said mutation, under conditions of specific hybridization between said probe and the mutant sequence to be detected, and detecting the hybridization complex.

24) (Amended) A method for obtaining a pair of primers allowing to detect a genetic polymorphic marker linked to a nucleic acid sequence encoding a polypeptide of claim 1, wherein said process comprises:

- a) screening a genomic DNA library from a vertebrate with a probe specific for a nucleic acid sequence encoding said polypeptide in order to select clones comprising said nucleic acid sequence and flanking chromosomal sequences;
- b) identifying a polymorphic locus in said flanking chromosomal sequences, and sequencing a DNA segment comprising said polymorphic locus; and
- c) designing primer pairs flanking said polymorphic locus.

25) (Amended) A method of claim 24 wherein the selected clones comprise at least a portion of a nucleic acid sequence encoding said polypeptide and up to 500 kb of a 3' and/or of a 5' adjacent sequence.

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26) (Amended) A method of claim 21 wherein the vertebrate is a mammal.

27) A method of claim 26 wherein said mammal is a pig.

Claims 28 – 29 have been amended

28) (Amended) A pair of primers obtainable by the process of claim 24.

29) (Amended) A process for detecting a dysfunction of carbohydrate metabolism resulting from the expression of a functionally altered allele of a polypeptide of claim 1 in a vertebrate, wherein said process comprises:

- a) obtaining a sample of genomic DNA from said vertebrate;
- b) contacting said DNA with a pair of primers under conditions allowing PCR amplification; and
- c) analyzing the PCR product to detect if an allele of a polymorphic marker linked to a nucleic acid sequence encoding a functionally altered allele of said polypeptide is present.

30) A process of claim 29, wherein said functionally altered polypeptide results from a R41Q substitution in SEQ ID NO: 2.

Claim 31 has been amended

31) (Amended) A process of claim 30, wherein said vertebrate is a mammal.

32) A process of claim 31 wherein said mammal is a pig.

Claim 33 has been amended

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33) (Amended) A process of claim 32 wherein the pair of primers is selected from the group consisting of

- a pair of primers consisting of SEQ ID NO: 5 and SEQ ID NO: 6;
- a pair of primers consisting of SEQ ID NO: 7 and SEQ ID NO: 8;
- a pair of primers consisting of SEQ ID NO: 9 and SEQ ID NO: 10;
- a pair of primers consisting of SEQ ID NO: 11 and SEQ ID NO: 12;
- a pair of primers consisting of SEQ ID NO: 13 and SEQ ID NO: 14;
- a pair of primers consisting of SEQ ID NO: 15 and SEQ ID NO: 16;
- a pair of primers consisting of SEQ ID NO: 17 and SEQ ID NO: 18;
- a pair of primers consisting of SEQ ID NO: 19 and SEQ ID NO: 20;
- a pair of primers consisting of SEQ ID NO: 21 and SEQ ID NO: 22;
- a pair of primers consisting of SEQ ID NO: 23 and SEQ ID NO: 24; and
- a pair of primers consisting of SEQ ID NO: 25 and SEQ ID NO: 26. --

Claims 34 – 37 have been canceled